

# FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGTCTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCCACAGCCTCAGATACTGGGGACTTTAC  
AGTCCCACAGAAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAAATGAGGCGCAGCGGGA  
AGCTCATTGTCAGACAAAGGCAAGTCTCTTTTCTCTCTCTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTGCAC  
CAATTTAGCAAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTGGGGTTG  
TTTCTCAGAGGGAACAACTACATTGTCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG  
ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCTATTTTCTGGGTCTCTACCCGCCAAACCGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCGCCCAAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAGTGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCTCGTGTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTATTACCTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATGAACTAAAAAACAACCTCGATTTTCAAAAACTTCAGTCTCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACAGCCCCAAT  
ACCTGAGAACCGCGCTGAAACTGTGTTTGCACCTTTTTCAGTGTTCAGATCTTGATTCCAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTACAGGAGGATCTACCTTCTCTGAAAATCCGCGGAA  
AACTTTTACACCTTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCTCAATGACTTTGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAAACGCTCCCGCCTTACCCAAAACCTCTACACCTCTTCGTC  
CGCGAGAAACAACAGCCCCGCGCTGCACATCCGCGAGCGTCAAGCGCTACAGACAGAGACTCAGG  
CACCACGCGCCAGGTCACTACTCGCTGCTGCCGCCAGGACCCGACCTCGCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGCGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCAGCGCTCCCGCGCGCTGAGCAG  
CGAGGCGCTGGTGCAGTGGTGGTGTCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACCGCTCCGCGCCCTGCAACGAGCTGGTGCCCGGGCGCGCGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACCGCTGGCTGTCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCGGCGCGCACAAATGGCGAGGTGCGCGA  
CGCCAGGCTGTCTGAGCGAGCGCGACGCGGCCAAGCAGAGCTGGTGGTGTGGTCAAGGAC  
AATGGCGAGCTCCGCGCTCGGCCACCGCCACGCTGCACGTCTCTGGTGGACGGCTTCTC  
CAGCCCTACCTGCTCTCTCCGGAGGCGGCCGACCCAGGCCAGGCCAGGCCGACTTGTCTACCG  
TCTACTGGTGGTGGCGTGTGGCTCGGTGCTCTCGCTCTCTCTCTTTTGGTGTCTCTGTTT  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGCGCGCTCGGTGGGTGCTGCTGGTGGCGCGA  
GGGCCCCCTTCAGGGGCATCTTGTGGACATGAGCGGCACCCAGGACCTATCCAGAGCTACC  
AGTATGAGGTGTCTGGCAGGAGGCTCAGGGAACCAATGAGTTCAAGTTCTCTGAAGCCGAT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCAGTGCACCATAGTTGACTTTTACATTTCCATAGGTATTTTATT  
TGTGCACTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSLFLLGLSLAGAAEPRSYSVVEETEGSSSFVTNLAKDLGLEQREFSR  
RGVRVVSRRGNKLHLQLNQETADLLLNKLDREDLCGHTEPCVLRQVLLSEPFQAEQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPVLVDKALDREEEAELRLTLTALDGGSPPRSQTAVYIEVLVDNDNAPEFEQPFY  
RVQISEDSPVGFVLVVKVSATDVTGVTGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVVTMSAFTSPIPENAPETVVVLFVS  
DLDSGKNGKISCSIQEDLPFLLKSAENFYTLTERPLDRESAEYNTITVTDLGTPMLITQ  
LNMVTLIADVNDNAPAFQTQTSYTLFVRENNSPALHRSVSATDRDSGTNAQVTVYSLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYELQGFQFRVGASDHGSPALSSEALVRVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATELGFGVWAH  
NGEVTRTARLLSERDAAKHRLVLVVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTAQ  
ADLLTVYLVVALASVSSLFVSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGSGGTNEFKFLKPIIPNFPQCPCGKEIQNSTFPNNFGFNQ

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

09978295-101501

## FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCTGGGCAATGGTCCCGGTGCGCGTGCACGCGCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTCAGAGGAAAGTGGTGCCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCATGTGTGATGCTGTCTG  
TGATTCTCTGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAAGTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCTTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTCTACCAGTTTGGCACCCGTAGC  
TGTTCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAGAAGAAT  
GTGGTGGTAACCTCAAGCCGACCAAATAGGCCCTCTTCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCTTATCTTTTAAATAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACCTCAATCCTTCGTTTCAGAAATAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

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